

DEX-0075

RAW SEQUENCE LISTING
ERROR REPORT

Docket System ✓
Status Report ✓
Docket Book ✓

BIOTECHNOLOGY
SYSTEMS
BRANCH

0500
SEP 21 2000

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

09/618,596

Source:

OIFE

Date Processed by STIC:

7/28/2000

9-13-2000

10-13-2000

(MAX) 3-13-2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/618,596

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ **Wrapped Nucleics** The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

- 2 ☐ **Wrapped Aminos** The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

- 3 ☐ **Incorrect Line Length** The rules require that a line not exceed 72 characters in length. This includes spaces.

- 4 ☐ **Misaligned Amino Acid Numbering** The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

- 5 ☐ **Non-ASCII** This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

- 6 ☐ **Variable Length** Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.

- 7 ☐ **PatentIn ver. 2.0 "bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

- 8 ☐ **Skipped Sequences (OLD RULES)** Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS: (Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

- 9 ☐ **Skipped Sequences (NEW RULES)** Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

- 10 ☒ **Use of n's or Xaa's (NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 11 ☐ **Use of <213>Organism (NEW RULES)** Sequence(s) _____ are missing this mandatory field or its response.

- 12 ☐ **Use of <220>Feature (NEW RULES)** Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

- 13 ☐ **PatentIn ver. 2.0 "bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/618,596

DATE: 07/28/2000
TIME: 14:55:17

Input Set : A:\Dex-0075.app
Output Set: N:\CRF3\07282000\I618596.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Macina, Roberto A.
4 Sun, Yongming
6 <120> TITLE OF INVENTION: A Novel Method of Diagnosing, Monitoring, Staging,
7 Imaging and Treating Colon Cancer
9 <130> FILE REFERENCE: DEX-0075
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/618,596
C--> 12 <141> CURRENT FILING DATE: 2000-07-17
14 <150> PRIOR APPLICATION NUMBER: 60/086,266
15 <151> PRIOR FILING DATE: 1998-05-21
17 <150> PRIOR APPLICATION NUMBER: PCT/US99/10498
18 <151> PRIOR FILING DATE: 1999-05-12
20 <160> NUMBER OF SEQ ID NOS: 1
22 <170> SOFTWARE: PatentIn Ver. 2.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 2608
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
29 <400> SEQUENCE: 1
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31 ctcttggggg aggtgtgtgt ttttcacatc ttaaaggctc acagaccctg cgtgtggcaa 120
32 atgttccatt cctgaaggac ctctccagaa tccggattgc tgaatcttcc ctgttgccaa 180
33 gaagggtccc aaaccacctc ttgacaatgg gaaactgggt ggtaaccac tggttttcag 240
34 ttttgtttct ggttgtttgg ttagggtcga atgttttctt gtttgtggat gccttctcga 300
35 aatatgagaa ggcgcagaaa tactactaca caagaaaaat ccttgggtga acattggcct 360
36 gtgcccgcgc gctgtctctc tgcctgaatt ttaacagcac gctgacctg cttcctgtgt 420
37 gtcgcaatct gctgtccttc ctgaggggca cctgctcatt ttgcagccgc acactgagaa 480
38 agcaattgga tcacaacctc accttccaca agctgggtgc ctatatgatc tgcctacata 540
39 cagctattca catcattgca cacctgttta actttgactg ctatagcaga agccgacagg 600
40 ccacagatgg ctcccttgc tccattctct ccagcctatc tcatgatgag aaaaaggggg 660
41 gttcttggct aaatcccac cagtcccga acacgacagt ggagtatgt acattcacca 720
42 gcgttgctgg tctcactgga gtgatcatga caatagcctt gattctcatg gtaacttcag 780
43 ctactgagtt catccggagg agttattttg aagtcttctg gtatactcac caccttttta 840
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50 tctctctcct ggaatggcat ccttttactt tgacctctgc tccagaggaa gatttcttct 1260
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53 ttttccagta tgaagtggct gtgctggttg gagcagggaat tggggtcacc ccctttgctt 1440
54 ctatcttgaa atccatctgg tacaaattcc agtgtgcaga ccacaacctc aaaacaaaaa 1500
55 agatctatct ctactggatc tgcagggaga cagggtccct ttcctgggtc aacaacctgt 1560
56 tgacttccct ggaacaggag atggagggaat taggcaaagt gggttttcta aactaccgtc 1620
57 tcttctcac cggatgggac agcaatattg ttggtcatgc agcattaaac tttgacaagg 1680
58 ccactgacat cgtgacaggc ctgaacagaa aaacctcctt tgggagacca atgtgggaca 1740

P. 2

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/618,596

DATE: 07/28/2000

TIME: 14:55:17

Input Set : A:\Dex-0075.app

Output Set: N:\CRF3\07282000\I618596.raw

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59 atgagttttc tacaatagct acctcccacc ccaagtctgt agtgggagtt ttcttatgtg 1800
60 gccctcggac tttggcaaaag agcctgcgca aatgctgtca ccgatattcc agtctggatc 1860
61 ctagaaaggt tcaattctac ttcaacaaag aaaatttttg agttatagga ataaggacgg 1920
62 taatctgcat tttgtctctt tgtatcttca gtaattgagt tataggaata aggacggtaa 1980
W--> 63 tctgcatttt gtctctttgt atcttcagta atttacttgg tctcttcagg tttgacagtt 2040
64 cacttttagat aagaatgtgc ctctcaagcc ttgactccct ggtattcttt ttttgattgc 2100
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68 caggtgattt tatcaattcc agtgttacca tctcctgagt tttgggttgg aatcttttgg 2340
69 ccctcccacc cccacagaag attttaagta gggtgacttt ttaaataaaa atttattgaa 2400
70 taattaatga taaaacataa taataaacat aaataataaa caaaattacc gagaacccca 2460
71 tccccatata acaccaacag tgtacatggt tactgtcact tttgatatgg tttatccagt 2520
72 gtgaacagca atttattatt tttgctcacc aaaaaataaa ggattttttt tcacttgaaa 2580
73 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa

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see item 10 on
Ena Summary
Sheet

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/618,596

DATE: 07/28/2000

TIME: 14:55:18

Input Set : A:\Dex-0075.app

Output Set: N:\CRF3\07282000\I618596.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number
 L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:63 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
 L:63 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
 L:63 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
 L:63 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
 L:63 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1
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 M:340 Repeated in SeqNo=1
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